

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:09:42 ; Search time 4177.15 Seconds
(without alignments)
9795.148 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagagaacgcggggc.....caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

SEQ 19 in
DNA databases

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match Length	DB	ID	%	
	1	944	100.0	6727	1	SCO007731	AJ007731 Streptomy
c	2	944	100.0	290850	1	SCO939127	AL939127 Streptomy
c	3	513.6	54.4	1203	1	STMAFSAA	M24250 S.griseus a
c	4	513.6	54.4	12070	1	AB011413	AB011413 Streptomy
c	5	279	29.6	6252	1	SVU24659	U24659 Streptomyce
c	6	272.4	28.9	1215	1	AB001608	AB001608 Streptomy
c	7	254	26.9	210614	1	AB088224	AB088224 Streptomy
c	8	208.2	22.1	2234	1	AB001683	AB001683 Streptomy
c	9	178.2	18.9	92294	1	AY117439	AY117439 Streptomy
	10	121.4	12.9	300550	1	AP005030	AP005030 Streptomy
	11	95.2	10.1	9521	6	AX188771	AX188771 Sequence
c	12	95.2	10.1	9521	6	AX188772	AX188772 Sequence
	13	95.2	10.1	22918	1	SCO276673	AJ276673 Streptomy
c	14	95.2	10.1	178073	1	SCO590464	AL590464 Streptomy
c	15	74.6	7.9	299050	1	SCO939119	AL939119 Streptomy
c	16	70.6	7.5	181850	2	BX276102	BX276102 Danio rer
c	17	69.8	7.4	125020	9	AF429315	AF429315 Homo sapi
	18	69.6	7.4	293050	1	SCO939116	AL939116 Streptomy
c	19	69.4	7.4	300425	1	AP005022	AP005022 Streptomy
c	20	68.8	7.3	4725	6	AX697993	AX697993 Sequence
c	21	68.8	7.3	60196	6	AX697977	AX697977 Sequence
	22	68.4	7.2	299425	1	AP005037	AP005037 Streptomy
c	23	68.4	7.2	303450	1	SCO939130	AL939130 Streptomy
c	24	68	7.2	166634	2	AC141736	AC141736 Apis mell
c	25	67.6	7.2	64790	8	AP004863	AP004863 Oryza sat
c	26	67	7.1	15738	6	AX803762	AX803762 Sequence
c	27	67	7.1	61944	6	AX803750	AX803750 Sequence
	28	67	7.1	125020	9	AF429315	AF429315 Homo sapi
c	29	66.4	7.0	48000	1	POL505006	AJ505006 Sorangium
c	30	66.4	7.0	172650	2	AP005772	AP005772 Oryza sat
c	31	66.2	7.0	8113	14	HSBBICP4A	L14320 Bovine herp
	32	66.2	7.0	135301	14	BHV1CGEN	AJ004801 Bovine he
c	33	66.2	7.0	135301	14	BHV1CGEN	AJ004801 Bovine he

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:08:32 ; Search time 696.032 Seconds
(without alignments)
5761.655 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaaacgcggggc.....caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	944	100.0	4346	6 ABN86379	Abn86379 ScbA, Scb
	2	944	100.0	4346	9 ADE14794	Adel4794 Streptomy
	3	170	18.0	401	6 ABN86377	Abn86377 S. coelic
c	4	170	18.0	401	6 ABN86378	Abn86378 S. coelic
	5	170	18.0	401	9 ADE14790	Adel4790 Streptomy
	6	95.2	10.1	9521	4 AAS07627	Aas07627 Streptoco
c	7	82	8.7	114955	2 AAX53491	Aax53491 Human ade
	8	75.8	8.0	114955	2 AAX53491	Aax53491 Human ade

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:18:52 ; Search time 157.972 Seconds
(without alignments)
3316.252 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaaacgcggggc.....caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
c 1	58.4	6.2	933	4	US-09-084-669-1	Sequence 1, Appli	
c 2	57.8	6.1	1908	1	US-08-173-508-1	Sequence 1, Appli	
c 3	57.8	6.1	1908	2	US-08-265-310-1	Sequence 1, Appli	
c 4	57.8	6.1	1908	3	US-08-951-742-1	Sequence 1, Appli	
5	56.8	6.0	1910	5	PCT-US92-05532-1	Sequence 1, Appli	
6	56.8	6.0	2261	1	US-08-272-882D-1	Sequence 1, Appli	
c 7	55.6	5.9	1044	1	US-07-975-526-3	Sequence 3, Appli	
c 8	55.6	5.9	1044	4	US-07-974-409C-425	Sequence 425, App	
9	55.6	5.9	30001	1	US-08-125-468-1	Sequence 1, Appli	
10	55.6	5.9	30001	2	US-08-474-933-1	Sequence 1, Appli	
c 11	54.4	5.8	2634	3	US-08-941-936-1	Sequence 1, Appli	
c 12	53.6	5.7	13842	3	US-09-105-537-30	Sequence 30, Appli	

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 02:55:38 ; Search time 2565.84 Seconds
(without alignments)
1288.292 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaaacgcggggc.....caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	944	100.0	4346	14	US-10-017-471A-19	Sequence 19, Appl
2	170	18.0	401	14	US-10-017-471A-12	Sequence 12, Appl
c 3	170	18.0	401	14	US-10-017-471A-13	Sequence 13, Appl
c 4	121.4	12.9	1035	14	US-10-156-761-2256	Sequence 2256, Ap
5	121.4	12.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 6	69.4	7.4	2817	14	US-10-156-761-390	Sequence 390, App
c 7	69.4	7.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 8	68.8	7.3	4725	14	US-10-205-032-17	Sequence 17, Appl
c 9	68.8	7.3	60196	14	US-10-205-032-1	Sequence 1, Appli
c 10	67	7.1	15738	14	US-10-329-079-46	Sequence 46, Appl
c 11	67	7.1	61944	14	US-10-329-079-34	Sequence 34, Appl
c 12	62.8	6.7	88421	9	US-09-976-059-1	Sequence 1, Appli
c 13	62.2	6.6	1674	15	US-10-369-493-31436	Sequence 31436, A
c 14	61.6	6.5	1869	14	US-10-156-761-6969	Sequence 6969, Ap
c 15	61.2	6.5	15738	14	US-10-329-079-12	Sequence 12, Appl
c 16	61.2	6.5	37360	14	US-10-329-079-6	Sequence 6, Appli
c 17	61	6.5	1296	14	US-10-156-761-3664	Sequence 3664, Ap
c 18	60.6	6.4	2406	15	US-10-369-493-42365	Sequence 42365, A
c 19	60.4	6.4	1200	14	US-10-156-761-6339	Sequence 6339, Ap
c 20	58.4	6.2	903	14	US-10-121-988-81	Sequence 81, Appl
c 21	58.4	6.2	903	14	US-10-200-562-81	Sequence 81, Appl
c 22	58.4	6.2	903	14	US-10-237-551-81	Sequence 81, Appl
c 23	58.4	6.2	927	14	US-10-121-988-83	Sequence 83, Appl
c 24	58.4	6.2	927	14	US-10-200-562-83	Sequence 83, Appl
c 25	58.4	6.2	927	14	US-10-237-551-83	Sequence 83, Appl
26	58.4	6.2	154746	10	US-09-827-688-8	Sequence 8, Appli
c 27	58.2	6.2	1942	12	US-10-282-122A-14251	Sequence 14251, A
c 28	58	6.1	1227	14	US-10-156-761-7107	Sequence 7107, Ap
c 29	58	6.1	2436	14	US-10-156-761-7456	Sequence 7456, Ap
c 30	57.8	6.1	31263	12	US-10-282-122A-25447	Sequence 25447, A
31	57.6	6.1	897	14	US-10-156-761-6477	Sequence 6477, Ap
c 32	57.4	6.1	2223	14	US-10-156-761-7068	Sequence 7068, Ap
c 33	57	6.0	1182	14	US-10-156-761-1195	Sequence 1195, Ap
34	57	6.0	2601	14	US-10-156-761-391	Sequence 391, App
c 35	57	6.0	10002	12	US-10-282-122A-14471	Sequence 14471, A
c 36	57	6.0	135638	14	US-10-314-657-1	Sequence 1, Appli
c 37	56.8	6.0	1284	14	US-10-156-761-6164	Sequence 6164, Ap
38	56.8	6.0	2934	14	US-10-156-761-3186	Sequence 3186, Ap
c 39	56.2	6.0	3282	14	US-10-156-761-3885	Sequence 3885, Ap
c 40	56.2	6.0	4833	12	US-10-282-122A-25605	Sequence 25605, A
c 41	55.8	5.9	1767	14	US-10-156-761-4150	Sequence 4150, Ap
42	55.6	5.9	1059	15	US-10-369-493-42237	Sequence 42237, A
c 43	55.6	5.9	1891	9	US-09-969-708-146	Sequence 146, App
c 44	55.6	5.9	1891	14	US-10-007-926A-234	Sequence 234, App
45	55.2	5.8	1554	12	US-10-282-122A-14450	Sequence 14450, A

ALIGNMENTS

RESULT 1
US-10-017-471A-19

5.1.6

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:18:08 ; Search time 6006.75 Seconds
(without alignments)
4693.036 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaaacgcggggc.....caaaactactgcttcggggca 944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	97.6	10.3	982	13	BX415111	BX415111	BX415111
2	81.2	8.6	976	29	AG030647	AG030647	Pan trogl
3	79	8.4	925	29	CNS0091P	AL053013	Drosophil
c 4	78.6	8.3	1421	28	BZ569488	BZ569488	pacs2-164
c 5	75.8	8.0	925	29	CNS0091P	AL053013	Drosophil
c 6	75.8	8.0	982	13	BX415111	BX415111	BX415111
c 7	75.6	8.0	1452	29	AG032979	AG032979	Pan trogl
c 8	75.2	8.0	1341	29	AG030611	AG030611	Pan trogl
c 9	75.2	8.0	1798	29	AG171124	AG171124	Pan trogl
c 10	74.8	7.9	1070	28	BZ557810	BZ557810	pacs1-60
11	73.8	7.8	932	29	CNS0072Q	AL066742	Drosophil
c 12	73.6	7.8	1073	14	CK209412	CK209412	FGAS02117
c 13	73.2	7.8	1299	29	AG039481	AG039481	Pan trogl
c 14	73	7.7	1165	29	AG030649	AG030649	Pan trogl
c 15	72.8	7.7	1189	29	AG030608	AG030608	Pan trogl
16	72.8	7.7	1598	29	AG030579	AG030579	Pan trogl
17	72.6	7.7	1370	29	AG072551	AG072551	Pan trogl
c 18	72	7.6	1143	13	BU502934	BU502934	AGENCOURT
c 19	71.6	7.6	1088	29	AG075424	AG075424	Pan trogl
20	71	7.5	796	28	AZ192927	AZ192927	SP_1022_B
21	70.8	7.5	1069	13	BQ675554	BQ675554	AGENCOURT
c 22	70.8	7.5	1277	29	AG060206	AG060206	Pan trogl
23	70.4	7.5	1250	29	AG043469	AG043469	Pan trogl
c 24	70	7.4	935	29	CNS006XK	AL066051	Drosophil
c 25	70	7.4	1040	12	BG786331	BG786331	SEAUMC006
c 26	69.8	7.4	932	29	CNS0072Q	AL066742	Drosophil
c 27	69.6	7.4	1203	29	CNS015Y4	AL106054	Drosophil
28	69.2	7.3	924	13	BX442207	BX442207	BX442207
29	69.2	7.3	1278	29	AG060116	AG060116	Pan trogl
30	69.2	7.3	1299	29	AG039481	AG039481	Pan trogl
c 31	69	7.3	1278	29	AG060116	AG060116	Pan trogl
c 32	68.8	7.3	1065	13	BQ681076	BQ681076	AGENCOURT
33	68.6	7.3	935	29	CNS006XK	AL066051	Drosophil
c 34	68.6	7.3	1369	29	AG081191	AG081191	Pan trogl
c 35	68.4	7.2	840	29	AG043467	AG043467	Pan trogl
36	68.4	7.2	1856	29	AG072699	AG072699	Pan trogl
c 37	67.8	7.2	1305	12	BM903696	BM903696	AGENCOURT
c 38	67.4	7.1	1135	13	BU506367	BU506367	AGENCOURT
39	67.2	7.1	1002	29	AG146122	AG146122	Pan trogl
40	67	7.1	1057	29	CNS046BO	AL276477	Tetraodon
41	66.8	7.1	1017	29	AG058770	AG058770	Pan trogl
c 42	66.8	7.1	1026	28	BZ569417	BZ569417	pacs2-164
c 43	66.8	7.1	1094	29	AG036373	AG036373	Pan trogl
44	66.8	7.1	1341	29	AG030611	AG030611	Pan trogl
c 45	66.6	7.1	1038	29	AG060254	AG060254	Pan trogl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 08:03:40 ; Search time 3439 Seconds
(without alignments)
3944.859 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.....GHQDGS LVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

*SEQ 17 (protein)
in DNA databases*

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101401_28710/app_query.fasta_1.455

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471_@CGN_1_1_5265_@runat_23022004_101401_28710 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*

```

12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	1634.5	99.4	6727	1	SCO007731		AJ007731	Streptomy
	2	1634.5	99.4	290850	1	SCO939127		AL939127	Streptomy
	3	1050.5	63.9	1203	1	STMAFSAA		M24250	S.griseus a
	4	1050.5	63.9	12070	1	AB011413		AB011413	Streptomy
	5	617	37.5	6252	1	SVU24659		U24659	Streptomyce
	6	562.5	34.2	1215	1	AB001608		AB001608	Streptomy
	7	524.5	31.9	210614	1	AB088224		AB088224	Streptomy
	8	510	31.0	92294	1	AY117439		AY117439	Streptomy
	9	483.5	29.4	2234	1	AB001683		AB001683	Streptomy
c	10	319.5	19.4	300550	1	AP005030		AP005030	Streptomy
c	11	271.5	16.5	9521	6	AX188771		AX188771	Sequence
	12	271.5	16.5	9521	6	AX188772		AX188772	Sequence
c	13	271.5	16.5	22918	1	SCO276673		AJ276673	Streptomy
	14	271.5	16.5	178073	1	SCO590464		AL590464	Streptomy
c	15	132	8.0	303400	1	AP006578		AP006578	Gloeobact
c	16	131	8.0	1755	1	STMBARA		D32251	Streptomyce
c	17	124.5	7.6	11426	1	AY271660		AY271660	Actinomad

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 07:58:09 ; Search time 397 Seconds
(without alignments)
3349.335 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.....GHQDGSVLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101401_28700/app_query.fasta_1
.455

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blösum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471 @CGN_1_1_708 @runat_23022004_101401_28700 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Query	Length				
c	1	1634.5	99.4	4346	6	ABN86379		Abn86379	ScbA, Scb
c	2	1634.5	99.4	4346	9	ADE14794		Adel4794	Streptomy
c	3	288	17.5	401	6	ABN86377		Abn86377	S. coelic
	4	288	17.5	401	6	ABN86378		Abn86378	S. coelic
c	5	288	17.5	401	9	ADE14790		Adel4790	Streptomy
c	6	271.5	16.5	9521	4	AAS07627		Aas07627	Streptoco
	7	126	7.7	3206	9	ADC30782		Adc30782	Human nov
	8	122	7.4	2971	5	AAS84741		Aas84741	DNA encod
	9	120	7.3	2492	9	ADD47157		Add47157	Human gen
	10	120	7.3	2492	9	ADE57663		Ade57663	Human gen
	11	120	7.3	2492	9	ADE57659		Ade57659	Human gen
	12	120	7.3	2492	9	ADD47153		Add47153	Human gen
c	13	119	7.2	2927	9	ADE59463		Ade59463	Human gen
	14	118.5	7.2	3131	9	ADC30783		Adc30783	Human nov
c	15	118.5	7.2	28000	9	ADD00956		Add00956	Human Jag
	16	115	7.0	1647	6	ABQ90156		Abq90156	M. capsul
	17	111.5	6.8	28598	2	AAT06769		Aat06769	Sorangium
	18	111.5	6.8	28958	2	AAT89956		Aat89956	Sorangium
	19	111.5	6.8	28958	3	AAA75299		Aaa75299	DNA seque
	20	111.5	6.8	49377	2	AAV05287		Aav05287	The sorap
c	21	109.5	6.7	5576	7	ACC48897		Acc48897	Rhodococc
c	22	109.5	6.7	23656	7	ACC48894		Acc48894	Rhodococc
c	23	108.5	6.6	77536	3	AAA14651		Aaa14651	Nucleotid
c	24	108	6.6	110000	4	AAI99682_38		Continuation (39 o	
c	25	108	6.6	110000	4	AAI99683_38		Continuation (39 o	
	26	108	6.6	135638	7	ABX34289		Abx34289	S. atrool
c	27	107.5	6.5	110000	4	AAI99683_20		Continuation (21 o	
	28	107	6.5	10763	2	AAV39837		Aav39837	Pseudomon
	29	107	6.5	10763	2	AAX99368		Aax99368	P. fluore
c	30	107	6.5	110000	4	AAI99682_20		Continuation (21 o	
	31	105.5	6.4	2081	2	AAV01452		Aav01452	Modified
	32	105.5	6.4	3196	2	AAV01447		Aav01447	Daunomyci
c	33	105.5	6.4	6491	6	ABA97234		Aba97234	pcu opero
c	34	105.5	6.4	6491	7	ACA92456		Aca92456	Pseudomon
	35	105	6.4	1384	4	AAS32671		Aas32671	Human gen
c	36	105	6.4	1644	9	ADC30402		Adc30402	Human nov
	37	104.5	6.4	3013	2	AAV01451		Aav01451	Plasmid p
	38	104.5	6.4	3196	2	AAV01453		Aav01453	Streptomy
c	39	104.5	6.4	3763	10	ADE77078		Ade77078	Human cDN
c	40	104.5	6.4	9975	7	AAL61173		Aal61173	Actinosyn
c	41	104.5	6.4	28598	2	AAT06769		Aat06769	Sorangium
c	42	104.5	6.4	28958	2	AAT89956		Aat89956	Sorangium
c	43	104.5	6.4	28958	3	AAA75299		Aaa75299	DNA seque
c	44	104.5	6.4	40123	9	ADB74388		Adb74388	Mycobacte
c	45	104.5	6.4	49377	2	AAV05287		Aav05287	The sorap

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 08:14:27 ; Search time 90 Seconds
(without alignments)
1929.996 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.....GHQDGSVLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101402_28736/app_query.fasta_1
.455

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471_@CGN_1_1_85_@runat_23022004_101402_28736 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	115.5	7.0	2127	4	US-09-252-991A-1503	Sequence 1503, Ap	
2	111.5	6.8	28958	1	US-08-258-261B-6	Sequence 6, Appli	
3	111.5	6.8	28958	1	US-08-456-837-6	Sequence 6, Appli	
4	111.5	6.8	28958	1	US-08-457-342-6	Sequence 6, Appli	
5	111.5	6.8	28958	1	US-08-457-646A-6	Sequence 6, Appli	
6	111.5	6.8	28958	1	US-08-458-076A-6	Sequence 6, Appli	
7	111.5	6.8	28958	1	US-08-764-233A-4	Sequence 4, Appli	
8	111.5	6.8	28958	1	US-08-457-335A-6	Sequence 6, Appli	
9	111.5	6.8	28958	1	US-08-729-214-6	Sequence 6, Appli	
10	111.5	6.8	28958	3	US-09-028-934-6	Sequence 6, Appli	
11	111.5	6.8	49377	1	US-08-764-233A-1	Sequence 1, Appli	
12	110	6.7	2250	4	US-09-252-991A-4181	Sequence 4181, Ap	
c 13	108.5	6.6	77536	4	US-09-410-551B-1	Sequence 1, Appli	
c 14	108	6.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli	
c 15	108	6.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
c 16	107	6.5	1251	4	US-09-489-039A-5971	Sequence 5971, Ap	
17	107	6.5	1443	4	US-09-252-991A-10228	Sequence 10228, A	
18	107	6.5	10763	1	US-08-761-258-1	Sequence 1, Appli	
19	107	6.5	10763	2	US-08-977-306-1	Sequence 1, Appli	
c 20	106.5	6.5	1266	4	US-09-252-991A-10804	Sequence 10804, A	
c 21	106	6.4	2730	4	US-09-489-039A-6744	Sequence 6744, Ap	
22	105.5	6.4	2081	2	US-09-096-982-7	Sequence 7, Appli	
23	105.5	6.4	2081	2	US-08-653-650A-7	Sequence 7, Appli	
24	105.5	6.4	3196	2	US-09-096-982-4	Sequence 4, Appli	
25	105.5	6.4	3196	2	US-08-653-650A-4	Sequence 4, Appli	
c 26	105.5	6.4	6491	4	US-09-585-174-1	Sequence 1, Appli	
c 27	104.5	6.4	2130	4	US-09-489-039A-3847	Sequence 3847, Ap	
28	104.5	6.4	3013	2	US-09-096-982-6	Sequence 6, Appli	
29	104.5	6.4	3013	2	US-08-653-650A-6	Sequence 6, Appli	
c 30	104.5	6.4	5185	4	US-09-976-594-640	Sequence 640, App	
c 31	104.5	6.4	28958	1	US-08-258-261B-6	Sequence 6, Appli	
c 32	104.5	6.4	28958	1	US-08-456-837-6	Sequence 6, Appli	
c 33	104.5	6.4	28958	1	US-08-457-342-6	Sequence 6, Appli	
c 34	104.5	6.4	28958	1	US-08-457-646A-6	Sequence 6, Appli	
c 35	104.5	6.4	28958	1	US-08-458-076A-6	Sequence 6, Appli	
c 36	104.5	6.4	28958	1	US-08-764-233A-4	Sequence 4, Appli	
c 37	104.5	6.4	28958	1	US-08-457-335A-6	Sequence 6, Appli	
c 38	104.5	6.4	28958	1	US-08-729-214-6	Sequence 6, Appli	
c 39	104.5	6.4	28958	3	US-09-028-934-6	Sequence 6, Appli	
c 40	104.5	6.4	40123	4	US-08-311-731A-137	Sequence 137, App	
c 41	104.5	6.4	49377	1	US-08-764-233A-1	Sequence 1, Appli	
42	104.5	6.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli	
43	104.5	6.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
44	104	6.3	1206	4	US-09-252-991A-16406	Sequence 16406, A	
45	104	6.3	1983	4	US-09-252-991A-16300	Sequence 16300, A	

ALIGNMENTS

RESULT 1

US-09-252-991A-1503

; Sequence 1503, Application US/09252991A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 09:26:05 ; Search time 383 Seconds
(without alignments)
2861.657 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.....GHQDGSVLVFLTTLSPAFSG 313

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101404_28819/app_query.fasta_1
.455

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10017471 @CGN_1_1_333 @runat_23022004_101404_28819
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	1634.5	99.4	4346	14	US-10-017-471A-19	Sequence 19, Appl
	2	319.5	19.4	1035	14	US-10-156-761-2256	Sequence 2256, Ap
c	3	319.5	19.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	4	288	17.5	401	14	US-10-017-471A-12	Sequence 12, Appl
	5	288	17.5	401	14	US-10-017-471A-13	Sequence 13, Appl
	6	118.5	7.2	2918	14	US-10-171-581-74	Sequence 74, Appl
c	7	118.5	7.2	28000	14	US-10-091-625-11	Sequence 11, Appl
c	8	118.5	7.2	28000	14	US-10-096-399A-11	Sequence 11, Appl
c	9	118.5	7.2	28000	15	US-10-461-668-11	Sequence 11, Appl
c	10	118.5	7.2	28000	15	US-10-388-263-381	Sequence 381, App
c	11	112.5	6.8	4062	14	US-10-156-761-875	Sequence 875, App
	12	110.5	6.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	13	109.5	6.7	1053	14	US-10-156-761-6354	Sequence 6354, Ap
	14	108.5	6.6	1219	15	US-10-374-780A-1144	Sequence 1144, Ap
c	15	108.5	6.6	77536	10	US-09-940-316B-1	Sequence 1, Appli
c	16	108	6.6	1704	14	US-10-156-761-963	Sequence 963, App
	17	108	6.6	135638	14	US-10-314-657-1	Sequence 1, Appli
	18	107.5	6.5	1101	15	US-10-369-493-31782	Sequence 31782, A
c	19	106.5	6.5	1785	14	US-10-156-761-3032	Sequence 3032, Ap
c	20	105.5	6.4	6491	9	US-09-997-664-1	Sequence 1, Appli
c	21	105.5	6.4	6491	15	US-10-464-952-1	Sequence 1, Appli
	22	105	6.4	1384	15	US-10-074-024-625	Sequence 625, App
	23	104.5	6.4	1821	14	US-10-156-761-1824	Sequence 1824, Ap
c	24	104.5	6.4	3763	10	US-09-919-039-243	Sequence 243, App
	25	104	6.3	13559	14	US-10-133-013-123	Sequence 123, App
	26	104	6.3	13793	15	US-10-159-563-110	Sequence 110, App
c	27	104	6.3	14427	14	US-10-156-761-1540	Sequence 1540, Ap
c	28	103.5	6.3	1120	16	US-10-294-445-22	Sequence 22, Appl
c	29	103.5	6.3	2166	12	US-10-282-122A-14878	Sequence 14878, A
	30	103	6.3	1137	14	US-10-156-761-1695	Sequence 1695, Ap
c	31	103	6.3	1248	14	US-10-156-761-1741	Sequence 1741, Ap
	32	103	6.3	1821	12	US-10-282-122A-26234	Sequence 26234, A
	33	103	6.3	1875	12	US-10-282-122A-28693	Sequence 28693, A
	34	103	6.3	3285	14	US-10-228-063-46	Sequence 46, Appl
c	35	103	6.3	4974	14	US-10-156-761-2487	Sequence 2487, Ap
	36	102.5	6.2	1219	15	US-10-369-493-35271	Sequence 35271, A
	37	102.5	6.2	1219	15	US-10-369-493-38541	Sequence 38541, A
	38	102.5	6.2	1219	15	US-10-369-493-38730	Sequence 38730, A
c	39	102.5	6.2	1803	14	US-10-156-761-3571	Sequence 3571, Ap
c	40	102.5	6.2	2076	12	US-10-282-122A-23281	Sequence 23281, A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 08:03:55 ; Search time 2549 Seconds
(without alignments)
3666.874 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.....GHQDGSVLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101402_28722/app_query.fasta_1.455

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471 @CGN_1_1_4237 @runat_23022004_101402_28722 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*

12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	125	7.6	1001	13	BQ056725	BQ056725 AGENCOURT
2	125	7.6	1086	13	BQ054980	BQ054980 AGENCOURT
3	123.5	7.5	1003	13	BQ056011	BQ056011 AGENCOURT
4	121.5	7.4	975	13	BQ060965	BQ060965 AGENCOURT
5	121.5	7.4	1051	13	BQ716861	BQ716861 AGENCOURT
6	121	7.4	1032	13	BQ069797	BQ069797 AGENCOURT
7	121	7.4	1060	12	BM909582	BM909582 AGENCOURT
8	120.5	7.3	921	13	BQ055424	BQ055424 AGENCOURT
9	120	7.3	940	13	BQ061849	BQ061849 AGENCOURT
10	120	7.3	947	13	BQ064227	BQ064227 AGENCOURT
11	120	7.3	948	13	BQ064307	BQ064307 AGENCOURT
12	120	7.3	984	13	BQ058735	BQ058735 AGENCOURT
13	120	7.3	986	13	BQ057095	BQ057095 AGENCOURT
14	120	7.3	990	13	BQ065162	BQ065162 AGENCOURT
15	120	7.3	991	13	BQ060878	BQ060878 AGENCOURT
16	120	7.3	1010	13	BQ059796	BQ059796 AGENCOURT
17	120	7.3	1037	13	BQ058702	BQ058702 AGENCOURT
18	120	7.3	1061	13	BQ061532	BQ061532 AGENCOURT
19	119.5	7.3	1054	13	BQ062294	BQ062294 AGENCOURT
20	119	7.2	930	13	BQ642458	BQ642458 AGENCOURT
21	119	7.2	1062	13	BQ062693	BQ062693 AGENCOURT
22	119	7.2	1067	13	BQ054981	BQ054981 AGENCOURT
23	118.5	7.2	883	29	CG232584	CG232584 OGWGZ16TV
24	118	7.2	552	14	CF135436	CF135436 UI-HF-BR0
25	118	7.2	725	14	CF125660	CF125660 UI-HF-EL0
26	118	7.2	862	13	BQ705954	BQ705954 AGENCOURT
27	118	7.2	1000	13	BQ071526	BQ071526 AGENCOURT
28	118	7.2	1051	12	BQ054446	BQ054446 AGENCOURT
29	117	7.1	1006	13	BQ068456	BQ068456 AGENCOURT